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## RAW SEQUENCE LISTING

DATE: 12/04/2001

PATENT APPLICATION: US/09/850,991

TIME: 13:25:26

Input Set : N:\Cr3\RULE60\09850991.txt

Output Set: N:\CRF3\12042001\I850991.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Kossmann, Jens

7 Willmitzer, Lothar

8 Emmermann, Michael

C--> 10 (ii) TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING

11 ENZYMES FROM MAIZE

13 (iii) NUMBER OF SEQUENCES: 4

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: FISH & NEAVE

17 (B) STREET: 1251 Avenue of the Americas

18 (C) CITY: New York

19 (D) STATE: New York

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 10020-1104

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/850,991

C--> 31 (B) FILING DATE: 08-May-2001

32 (C) CLASSIFICATION:

38 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 09/148,680

36 (B) FILING DATE: 1998-09-04

39 (A) APPLICATION NUMBER: DE 196 08 918.2

40 (B) FILING DATE: 07-MAR-96

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Haley Jr., James F.

44 (B) REGISTRATION NUMBER: 27,794

45 (C) REFERENCE/DOCKET NUMBER: GFB-7

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: (212) 596-9000

49 (B) TELEFAX: (212) 596-9090

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 1993 base pairs

55 (B) TYPE: nucleotide

56 (C) STRANDEDNESS: double

57 (D) TOPOLOGY: linear

59 (ii) MOLECULE TYPE: cDNA to mRNA

61 (iii) HYPOTHETICAL: NO

C--> 63 (iv) ANTI-SENSE: NO

65 (vi) ORIGINAL SOURCE:

66 (A) ORGANISM: Zea mays

ENTERED

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67          (F) TISSUE TYPE: Blattgewebe
69      (ix) FEATURE:
70          (A) NAME/KEY: CDS
71          (B) LOCATION:1..1675
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 GGC ACG AGG TCA AAA CTC CCT CCA GGG TCA GAT TTG CAA CAA GCT GCA      48
77 Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala
W--> 78      1          5          10          15
80 ATT GTG GCT ATT CAG GAA GAG GAC CCT TAT AAT TGG GGG TAT AAC CCT      96
81 Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro
82          20          25          30
84 GTG GTT TGG GGC GTT CCA AAA GGA AGC TAT GCA AGT AAC CCA GAT GGT      144
85 Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly
86          35          40          45
88 CCA AGT CGT ATC ATT GAG TAC CGG CTG ATG GTG CAG GCC TTG AAT CGC      192
89 Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg
90          50          55          60
92 TTA GGT CTT CGA GTT GTC ATG GAT GTT GTA TAC AAT CAT CTA TAC TCA      240
93 Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser
94      65          70          75          80
96 AGT GGC CCT TTT GCC ATC ACT TCC GTG CTT GAC AAG ATT GTA CCT GGA      288
97 Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly
98          85          90          95
100 TAC TAC CTC AGA AGG GAC TCT AAT GGT CAG ACT GAG AAC AGC GCG GCT      336
101 Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala
102          100          105          110
104 GTG AAC AAT ACA GCA AGT GAG CAT TTC ATG GTT GAT AGA TTA ATC GTG      384
105 Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val
106          115          120          125
108 GAT GAC CTT CTG AAT TGG GCA GTA AAT TAC AAA GTT GAC GGG TTC AGA      432
109 Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg
110          130          135          140
112 TTT GAT CTA ATG GGA CAT ATC ATG AAA AAG ACA ATG ATT AGA GCA AAA      480
113 Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
114 145          150          155          160
116 TCG GCT CTT CAA AGC CTT ACA ATT GAT GAA CAT GGA GTA GAT GGT TCA      528
117 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
118          165          170          175
120 AAG ATA TAC TTG TAT GGT GAA GGA TGG AAC TTC GGT GAA GTT GCG GAA      576
121 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu
122          180          185          190
124 AAT CAA CGT GGG ATA AAT GGA TCC CAG CTA AAT ATG AGT GGC ACT GGG      624
125 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
126          195          200          205
128 ATT GGT AGT TTC AAC GAT AGA ATC CGT GAT GCT ATA AAT GGT GGC AGT      672
129 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
130          210          215          220
132 CCG TTT GGG AAT CCA CTG CAA CAA GGT TTC TCT ACT GGA TTG TTC TTA      720
133 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu

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134	225		230		235		240	
136	GAG CCA AAT GGA TTT	TAT CAG GGC AAT GAA ACA GAG ACA AGG CTC ACG	768					
137	Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr							
138		245 250 255						
140	CTT GCT ACA TAC GCT GAC CAT ATA CAG ATT GGA TTA GCT GGC AAT TTG	816						
141	Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu							
142		260 265 270						
144	AAG GAC TAT GTA GTT ATA TCT CAT ACT GGA GAA GCT AGA AAA GGA TCT	864						
145	Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser							
146		275 280 285						
148	GAA ATT CGC ACC TTC GAT GGC TCA CCA GTT GGC TAT GCT TCA TCC CCT	912						
149	Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro							
150		290 295 300						
152	ATA GAA ACA ATA AAC TAC GCC TCT GCT CAT GAC AAT GAA ACA CTA TTT	960						
153	Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe							
154	305 310 315 320							
156	GAT ATT ATT AGT CTA AAG ACT CCG ATG GAC CTC TCA ATT GAC GAG CGA	1008						
157	Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg							
158		325 330 335						
160	TGC AGG ATA AAT CAT TTG TCC ACA AGC ATG ATT GCA TTA TCC CAG GGA	1056						
161	Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly							
162		340 345 350						
164	ATA CCA TTT TTT CAT GCT GGT GAT GAG ATA CTA CGA TCT AAG TCG CTT	1104						
165	Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu							
166		355 360 365						
168	GAT CGA GAT TCA TAT GAC TCT GGT GAT TGG TTT AAC AAG ATT GAT TTT	1152						
169	Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe							
170		370 375 380						
172	ACC TAT GAA ACA AAC AAT TGG GGT GTT GGG CTT CCA CCA AGA GAA AAG	1200						
173	Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys							
174	385 390 395 400							
176	AAC GAA GGG AGC TGG CCT TTG ATG AAG CCA AGA TTG GAG AAC CCG TCG	1248						
177	Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser							
178		405 410 415						
180	TTC AAA CCT GCA AAA CAT GAC ATT ATT GCT GCC TTA GAC AAA TTT ATT	1296						
181	Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile							
182		420 425 430						
184	GAT ATC CTC AAG ATC AGA TAC TCA TCA CCT CTC TTT CGC CTA ACT ACA	1344						
185	Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr							
186		435 440 445						
188	GCA AGT GAT ATT GTG CAA AGG GTT CAC TTT CAC AAC ACA GGG CCC TCC	1392						
189	Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser							
190		450 455 460						
192	TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT	1440						
193	Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp							
194	465 470 475 480							
196	AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA	1488						
197	Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr							
198		485 490 495						

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```

200 GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT      1536
201 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu
202          500          505          510
204 GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT      1584
205 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp
206          515          520          525
208 GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC      1632
209 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr
210          530          535          540
212 GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T      1675
213 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys
214 545          550          555
216 GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCGGCATC CAAGTCGAAG CAAACGAATG      1735
218 AAATAAGAGA AGGCCATCGA ATAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC      1795
220 CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAAATAAAT      1855
222 AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCT      1915
224 ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT      1975
226 AATTTTATGC AAAAAAAAAA      1993
229 (2) INFORMATION FOR SEQ ID NO: 2:
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 558 amino acids
233 (B) TYPE: amino acid
234 (D) TOPOLOGY: linear
236 (ii) MOLECULE TYPE: protein
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
240 Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala
241 1          5          10          15
243 Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro
244          20          25          30
246 Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly
247          35          40          45
249 Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg
250          50          55          60
252 Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser
253 65          70          75          80
255 Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly
256          85          90          95
258 Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala
259          100          105          110
261 Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val
262          115          120          125
264 Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg
265          130          135          140
267 Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
268 145          150          155          160
270 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
271          165          170          175
273 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu
274          180          185          190

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```

276 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
277      195      200      205
279 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
280      210      215      220
282 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu
283 225      230      235      240
285 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr
286      245      250      255
288 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu
289      260      265      270
291 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser
292      275      280      285
294 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro
295      290      295      300
297 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe
298 305      310      315      320
300 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg
301      325      330      335
303 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly
304      340      345      350
306 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu
307      355      360      365
309 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe
310      370      375      380
312 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys
313 385      390      395      400
315 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser
316      405      410      415
318 Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile
319      420      425      430
321 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr
322      435      440      445
324 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser
325      450      455      460
327 Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp
328 465      470      475      480
330 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr
331      485      490      495
333 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu
334      500      505      510
336 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp
337      515      520      525
339 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr
340      530      535      540
342 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys
343 545      550      555
346 (2) INFORMATION FOR SEQ ID NO: 3:
348      (i) SEQUENCE CHARACTERISTICS:
349          (A) LENGTH: 492 base pairs

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## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09850991.txt

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L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:63 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:358 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:380 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:401 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:409 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3